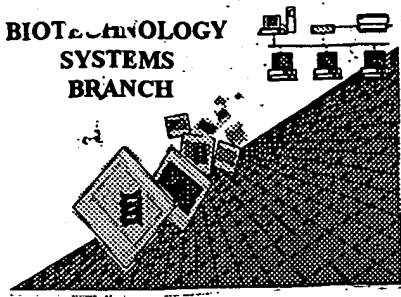


0570
0809

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/918,026
Source: O/PK
Date Processed by STIC: 8/7/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/918,026

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/918,026

DATE: 08/07/2001

TIME: 13:57:45

Input Set : A:\isph-588.txt

Output Set: N:\CRF3\08072001\I918026.raw

**Does Not Comply
Corrected Diskette Needed**

4 <110> APPLICANT: Rosanne M. Crooke
 5 Mark J. Graham
 6 Kristina M. Lemonidis
 9 <120> TITLE OF INVENTION: ANTISENSE MODULATION OF ACYL COA CHOLESTEROL
 ACYLTRANSFERASE-2 EXPRESSION
 11 <130> FILE REFERENCE: ISPH-0588
 OK 13 <140> CURRENT APPLICATION NUMBER: US/09/918,026
 13 <141> CURRENT FILING DATE: 2001-07-30
 13 <160> NUMBER OF SEQ ID NOS: 65

ERRORED SEQUENCES

987 <210> SEQ ID NO: 65
 988 <211> LENGTH: 20
 989 <212> TYPE: DNA
 990 <213> ORGANISM: Artificial Sequence
 992 <220> FEATURE:
 993 <223> OTHER INFORMATION: Antisense Oligonucleotide
 995 <400> SEQUENCE: 65
 996 ctaggtatgg caggaccaag 20
 E--> 999 1
 E--> 1002 18

delete - see next pages for more errors

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/918,026

DATE: 10/04/2001

TIME: 18:21:35

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10042001\I918026.raw

```

199 <400> SEQUENCE: 5
200 cccgggcacc aagga                                     15
202 <210> SEQ ID NO: 6
203 <211> LENGTH: 25
204 <212> TYPE: DNA
205 <213> ORGANISM: Artificial Sequence
207 <220> FEATURE:
208 <223> OTHER INFORMATION: PCR Probe
210 <400> SEQUENCE: 6
211 ctacgtgtat caggatgggc tgcgg                             25
213 <210> SEQ ID NO: 7
214 <211> LENGTH: 19
215 <212> TYPE: DNA
216 <213> ORGANISM: Artificial Sequence
218 <220> FEATURE:
219 <223> OTHER INFORMATION: PCR Primer
221 <400> SEQUENCE: 7
222 gaaggtgaag gtcggagtc                                     19
224 <210> SEQ ID NO: 8
225 <211> LENGTH: 20
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: PCR Primer
232 <400> SEQUENCE: 8
233 gaagatggtg atgggatttc                                   20
235 <210> SEQ ID NO: 9
236 <211> LENGTH: 20
237 <212> TYPE: DNA
238 <213> ORGANISM: Artificial Sequence
240 <220> FEATURE:
241 <223> OTHER INFORMATION: PCR Probe
243 <400> SEQUENCE: 9
244 caagcttccc gttctcagcc                                   20
246 <210> SEQ ID NO: 10
247 <211> LENGTH: 1607
248 <212> TYPE: DNA
249 <213> ORGANISM: Mus musculus
251 <220> FEATURE:
252 <221> NAME/KEY: CDS
253 <222> LOCATION: (30)...(1607)
255 <400> SEQUENCE: 10
256 ctgtgtgctg tccgctctac actggcacc atg cag cca aag gtg ccc cag ctt  53
257                                     Met Gln Pro Lys Val Pro Gln Leu
258                                     1                               5
260 cgg agg aga gaa ggg ctg gga gag gag cag gag aag gga gcc cgt gga  101
261 Arg Arg Arg Glu Gly Leu Gly Glu Glu Gln Glu Lys Gly Ala Arg Gly
262 10                               15                               20
264 gga gaa ggg aac gca agg aca cac gga acc cca gac ttg gtg caa tgg  149

```

see next page

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/918,026

DATE: 10/04/2001

TIME: 18:21:35

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\10042001\I918026.raw

W--> 265 Gly Glu Gly Asn Ala Arg Thr His Gly Thr Pro Asp Leu Val Gln Trp
266 25 30 35 40
268 act cga cat atg gag gct gtg aag acn cag ttt ctg gag caa gca cag 197
269 Thr Arg His Met Glu Ala Val Lys Thr Gln Phe Leu Glu Gln Ala Gln
270 45 50 55
272 aga gag ttg gca gag ctg ttg gat cgg gcc cta tgg gag gct atg caa 245
273 Arg Glu Leu Ala Glu Leu Leu Asp Arg Ala Leu Trp Glu Ala Met Gln
274 60 65 70
276 gct tac ccc aaa caa gac aga cct ctt ccc tcc gct gcc cca gat tct 293
277 Ala Tyr Pro Lys Gln Asp Arg Pro Leu Pro Ser Ala Ala Pro Asp Ser
278 75 80 85
280 aca agc aag acc ccg gag tta cgc cct gga aaa cgg aaa gtt ttc gtc 341
281 Thr Ser Lys Thr Pro Glu Leu Arg Pro Gly Lys Arg Lys Val Phe Val
282 90 95 100
284 gcc cgc aag tca ctg atc gat gag cta atg gag gtg caa cat ttc cga 389
285 Ala Arg Lys Ser Leu Ile Asp Glu Leu Met Glu Val Gln His Phe Arg
286 105 110 115 120
288 acc atc tac cac atg ttc ata gcg ggc cta tgg ttc ttg atc atc agc 437
289 Thr Ile Tyr His Met Phe Ile Ala Gly Leu Trp Phe Leu Ile Ile Ser
290 125 130 135
292 acc ctg gcc atc gac ttc att gat gag ggc agg ttg atg ctg gag ttt 485
293 Thr Leu Ala Ile Asp Phe Ile Asp Glu Gly Arg Leu Met Leu Glu Phe
294 140 145 150
296 gac tta ctc ctc ttc agc ttc gga cag ctg ccc ttg gcg ctg atg acc 533
297 Asp Leu Leu Leu Phe Ser Phe Gly Gln Leu Pro Leu Ala Leu Met Thr
298 155 160 165
300 tgg gtt ccc atg ttc ctg tat acg ctc cta gtg ccc tac cag acc ctg 581
301 Trp Val Pro Met Phe Leu Tyr Thr Leu Leu Val Pro Tyr Gln Thr Leu
302 170 175 180
304 tgg ctg tgg gcc agg ccg cgc gct ggg ggt gcc tgg atg ctg ggg gcc 629
305 Trp Leu Trp Ala Arg Pro Arg Ala Gly Gly Ala Trp Met Leu Gly Ala
306 185 190 195 200
308 agc ctg ggc tgc gtt ctg ctg gct gcc cac gct gtg gtg ctc tgc gtc 677
309 Ser Leu Gly Cys Val Leu Leu Ala Ala His Ala Val Val Leu Cys Val
310 205 210 215
312 ctg ccg gtg cac gtg tca gtg agg cat gag ctt ccg ccc gcc tcg cgc 725
313 Leu Pro Val His Val Ser Val Arg His Glu Leu Pro Pro Ala Ser Arg
314 220 225 230
316 tgc gtg ctg gtc ttt gag cag gtc aga ttg ctg atg aaa agc tac tcc 773
317 Cys Val Leu Val Phe Glu Gln Val Arg Leu Leu Met Lys Ser Tyr Ser
318 235 240 245
320 ttc ctg aga gag act gtg cct ggg atc ttt tgt gtc aga cga gga aag 821
321 Phe Leu Arg Glu Thr Val Pro Gly Ile Phe Cys Val Arg Arg Gly Lys
322 250 255 260
324 ggc atc agc ccc cca agt ttc tcc agc tac ctc tac ttc ctc ttc tgc 869
325 Gly Ile Ser Pro Pro Ser Phe Ser Ser Tyr Leu Tyr Phe Leu Phe Cys
326 265 270 275 280
328 cct aca ctt atc tac aga gag aca tac ccc agg aca ccc agc atc agg 917
329 Pro Thr Leu Ile Tyr Arg Glu Thr Tyr Pro Arg Thr Pro Ser Ile Arg

see
item 9
on Enol.
Summary
Sheet

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/918,026

DATE: 08/07/2001

TIME: 13:57:46

Input Set : A:\isph-588.txt

Output Set: N:\CRF3\08072001\I918026.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:268 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:10
L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:999 M:254 E: No. of Bases conflict, LENGTH:Input:1 Counted:20 SEQ:65
M:254 Repeated in SeqNo=65